

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lawrence, Geoffrey

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Ratner & Prestia
- (B) STREET: P.O. Box 980
- (C) CITY: Valley Forge
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To be assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 96 24677.2
- (B) FILING DATE: Filed November 27, 1996  
and
- (A) APPLICATION NUMBER: GB 9709463.5
- (B) FILING DATE: May 9, 1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Prestia, Paul F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH30170

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
TACCAACCAC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCCAT	GAAGAACCCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCC	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCGCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGGA	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAAC	TAAGATGCGT	TTTCACAGCC	AACTCTCTC	CCAGGACTGG	1080
CCACACCCTA	CCTTGTGTGT	GATGGCACAC	CAGAATGAAA	ACCCGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5				10				15			
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
				20				25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
				35			40				45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
				50			55				60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
				65			70			75			80		
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85			90			95					
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
				100			105			110					
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
				115			120			125					
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
				130			135			140					
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
				145			150			155			160		
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
				165			170			175					
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
				180			185			190					
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

195	200	205	
Glu Pro His Ala Gln Gly Leu	Leu Leu Cys Pro	Cys Ala Pro Asn Asp	
210	215	220	
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr	Ile Ala Pro Asn Cys Ala		
225	230	235	240
Leu Pro Pro Val Ala Pro Asn Cys Leu	Glu Leu Arg Arg Leu Cys Phe		
245	250	255	
Ser Asp Pro Leu Cys Arg Ser Arg	Leu Val Asp Phe Gln Thr His Cys		
260	265	270	
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr	Glu Gln Ser Arg Cys		
275	280	285	
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala	Met Thr Pro Asn Phe		
290	295	300	
Val Ser Asn Val Asn Thr Ser Val Ala Leu	Ser Cys Thr Cys Arg Gly		
305	310	315	320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met	Leu Glu Gly Phe Phe Ser		
325	330	335	
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala	Lys Met Arg Phe His		
340	345	350	
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro	Thr Phe Ala Val Met		
355	360	365	
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro	Gln Pro Trp Val Pro		
370	375	380	
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu	Leu Ser Leu Trp		
385	390	395	400

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGATGCC	180
TACCACCACC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGGCAT	GAAGAACCCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCCTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCC	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAACAGC	CGCCGAGCCC	CACGCCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCCAACA	CCATGCC	CAACTGCGCG	720
CTGCCGCCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCAGACCC	CACTGCCATC	CCATGGACAT	CCTAGGAAC	840
TGTGCAACAG	AGCAGTCCAG	ATGTCCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCC	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAGC	TAAGATGCCT	TTTCACAGCC	AACTCTCTC	CCAGGACTGG	1080
CCACACCCCTA	CCTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met  
1 5 10 15  
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp  
20 25 30  
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg  
35 40 45  
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu  
50 55 60  
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro  
65 70 75 80  
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser  
85 90 95  
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala  
100 105 110  
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn  
115 120 125  
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro  
130 135 140  
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp  
145 150 155 160  
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp  
165 170 175  
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln  
180 185 190  
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala  
195 200 205  
Glu Pro His Ala Gln Gly Leu Leu Cys Pro Cys Ala Pro Asn Asp  
210 215 220  
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala  
225 230 235 240  
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe  
245 250 255  
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys  
260 265 270  
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys  
275 280 285  
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe  
290 295 300  
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly  
305 310 315 320  
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser  
325 330 335  
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His  
340 345 350  
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met  
355 360 365  
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro  
370 375 380  
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp

385

390

395

400

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGCCGGC	GCAACACCAT	CGCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTTGCA	GATCACGCC	GGTGGATTTC	120
CAGACCCACT	GCCATCCCCT	GGACATCCTA	GGAACTTGTG	CAACAGAGCA	GTCCAGATGT	180
CTACGAGCAT	ACCTGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTGT	CAGCAATGTC	240
AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGGAGTGT	300
GAAATGCTGG	AAGGGTTCTT	CTCCCACAAAC	CCCTGCCTCA	CGGAGGCCAT	TGCAGCTAAG	360
ATGCGTTTC	ACAGCCAAC	CTTCTCCCAG	GACTGGCCAC	ACCCTACCTT	TGCTGTGATG	420
GCACACCAGA	ATGAAAACCC	TGCTGTGAGG	CCACAGCCCT	GGGTGCCCTC	TCTTTCTCC	480
TGCA	CCTGATTCT	GCTCCTGAGC	CTATGGTAG			519

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val
1				5				10				15			
Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu
				20				25				30			
Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp
				35				40			45				
Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr
				50				55			60				
Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val
				65				70			75			80	
Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu
				85				90			95				
Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys
				100				105			110				
Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe
				115				120			125				
Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn
				130				135			140				
Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser
				145				150			155			160	
Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Ser	Leu	Trp					
				165				170							

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lawrence, Geoffrey

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Ratner & Prestia
- (B) STREET: P.O. Box 980
- (C) CITY: Valley Forge
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To be assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 96 24677.2
- (B) FILING DATE: Filed November 27, 1996  
and
- (A) APPLICATION NUMBER: GB 9709463.5
- (B) FILING DATE: May 9, 1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Prestia, Paul F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH30170

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
TACCAACC	TGGATTCTTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGGCAT	GAAGAACCG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAAGAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAACGG	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGCGCACA	CCATGCC	CAACTGCGCG	720
CTGCCGCCTG	TGGCCCCAA	CTGCCTGGAG	CTGCAGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGA	TTTCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTC	CCAGGACTGG	1080
CCACACCC	CCTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5				10				15			
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
					20			25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
					35			40			45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
					50			55			60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
					65			70			75			80	
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
					85			90			95				
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
					100			105			110				
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
					115			120			125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
					130			135			140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
					145			150			155			160	
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
					165			170			175				
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
					180			185			190				
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

195                  200                  205

Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp  
 210                  215                  220  
 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala  
 225                  230                  235                  240  
 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe  
 245                  250                  255  
 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys  
 260                  265                  270  
 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys  
 275                  280                  285  
 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe  
 290                  295                  300  
 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly  
 305                  310                  315                  320  
 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser  
 325                  330                  335  
 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His  
 340                  345                  350  
 Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met  
 355                  360                  365  
 Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro  
 370                  375                  380  
 Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp  
 385                  390                  395                  400

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGATGCC	180
TACCAACCACC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCCT	GGAGGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCCCAT	GAAGAACCGAG	GTTGCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCGCAAAC	CCTGGAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCCTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCT	CAGGCAGCTG	600
CTCACTTCT	TCGAGAACGGC	CGCCGAGCCC	CACGCCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCCAAACA	CCATGCC	CAACTGCC	720
CTGCCGCCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAAC	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCAAAC	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met  
1 5 10 15  
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp  
20 25 30  
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg  
35 40 45  
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu  
50 55 60  
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro  
65 70 75 80  
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser  
85 90 95  
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala  
100 105 110  
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn  
115 120 125  
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro  
130 135 140  
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp  
145 150 155 160  
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp  
165 170 175  
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln  
180 185 190  
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala  
195 200 205  
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp  
210 215 220  
Arg Gly Cys Gly Glu Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala  
225 230 235 240  
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe  
245 250 255  
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys  
260 265 270  
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys  
275 280 285  
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe  
290 295 300  
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly  
305 310 315 320  
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser  
325 330 335  
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His  
340 345 350  
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met  
355 360 365  
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro  
370 375 380  
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Ser Leu Trp

385

390

395

400

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGCCGGC	GCAACACCAT	CGCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTGCA	GATCACGCC	GGTGGATTTC	120
CAGACCCACT	GCCATCCCAT	GGACATCCTA	GGAACTTGTG	CAACAGAGCA	GTCAGATGT	180
CTACGAGCAT	ACCTGGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTGT	CAGCAATGTC	240
AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGGAGTGT	300
GAAATGCTGG	AAGGGTTCTT	CTCCCACAAAC	CCCTGCCCTCA	CGGAGGCCAT	TGCAGCTAAG	360
ATGCGTTTC	ACAGCCAAC	CTTCTCCCAG	GACTGGCCAC	ACCCTACCTT	TGCTGTGATG	420
GCACACCAGA	ATGAAAACCC	TGCTGTGAGG	CCACAGCCCT	GGGTGCCCTC	TCTTTCTCC	480
TGCACGCTTC	CCTTGATTCT	GCTCCTGAGC	CTATGGTAG			519

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val
1				5				10				15			
Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu
				20				25				30			
Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp
				35				40			45				
Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr
				50				55			60				
Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val
				65				70			75			80	
Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu
					85				90			95			
Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys
				100				105			110				
Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe
				115				120			125				
Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn
				130				135			140				
Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser
				145				150			155			160	
Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp				
				165				170							

**Figure I - SEQ ID NO:1**

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT  
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC  
 101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG  
 151 TGCCAGGCTG ATCCCACCTG CAGTGCTGCC TACCACCACC TGGATTCCCTG  
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG  
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC  
 301 TGCATGTGCC ACCGGCGCAT GAAGAACAG GTTGCCTGCT TGGACATCTA  
 351 TTGGACCGTT CACCGTGCC GCAGCCTTGG TAACTATGAG CTGGATGTCT  
 401 CCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC  
 451 AAACGTAAACA TGCTCAAACC AGACTCAGAC CTCTGCCCTCA AGTTTGCCAT  
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG  
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGGCC ACGTCTGCCT CAGGCAGCTG  
 601 CTCACTTCTC TCGAGAAGGC CGCCGAGCCC CACCGCGCAGG GCCTGCTACT  
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA  
 701 CCATCGCCCC CAACTGCGCG CTGCCGCCCTG TGGCCCCCAA CTGCCTGGAG  
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAAGATCAC GCCTGGTGG  
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG  
 851 AGCAGTCCAG ATGTCTACGA GCATACTGG GGCTGATTGG GACTGCCATG  
 901 ACCCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCTTAAGCTGCAC  
 951 CTGCGGAGGC AGTGGCAACC TGCAAGGAGGA GTGTGAAATG CTGGAAGGGT  
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT  
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTGCTGT  
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC  
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

**Figure 2 - SEQ ID NO:2**

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK  
 51 CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG  
 101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL  
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL  
 201 LTFFEKAAP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE  
 251 LRRLCFSDPL CRSRLVDFQT HCHPMIDILGT CATEQSRLCLR AYLGLIGTAM  
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR  
 351 FHSQQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

**Figure 3 - SEQ ID NO:3**

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT  
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC  
 101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG  
 151 TGCCAGGCTG ATCCCACCTG CAGTGATGCC TACCACCACC TGGATTCTG  
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG  
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC  
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAAG GTTGCCTGCT TGGAcATCTA  
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT  
 401 CCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC  
 451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT  
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG  
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGGCC ACGTCTGCCT CAGGCAGCTG  
 601 CTCACTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT  
 651 GTGCCCATGT GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA  
 701 CCATCGCCCC CAACTGCGCG CTGCCGCCTG TGGCCCCAA CTGCCTGGAG  
 751 CTGGCGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA  
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG  
 851 AGCAGTCCAG ATGTCTACGA GCATACTGG GGCTGATTGG GACTGCCATG  
 901 ACCCCCAACT TTGTCAAGCAA TGTCAACACC AGTGTGCTCT TAAGCTGCAC  
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT  
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT  
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTGCTGT  
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC  
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

**Figure 4 - SEQ ID NO:4**

1 MVRPLNPRPL PPVVLMLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK  
 51 CQADPTCSDA YHLDSCSISTPLPSEEP SVPADCLEAA QQLRNSSLIG  
 101 CMCHRRMKNQ VACLDIYWTIV HRARSLGNYE LDVSPYEDTV TSKPWKMNL  
 151 KLNMLKPDSL LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL  
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCL  
 251 LRRLCFSDP CRSRLVDFQT HCHPMDILGT CATEQSRLR AYLGLIGTAM  
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR  
 351 FHSQQLFSQDW PHPTFAVMAM QNENPAVRPQ PWVPSLFSC LPLILLSLW

**Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF  $\alpha 3$  receptor)**

```

1      GAGCGCCGGC GCAACACCAT CGCCCCAAC TGCGCGCTGC CGCCTGTGGC
5
51     CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTGCA
101    GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA
10      151   GGAACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGGCT
201    GATTGGGACT GCCATGACCC CCAACTTGT CAGCAATGTC AACACCAGTG
251    TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT
15
301    GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT
351    TGCAGCTAAG ATGCGTTTC ACAGCCAAC TTTCTCCAG GACTGGCCAC
20      401   ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG
451     CCACAGCCCT GGGTGCCCTC TCTTTCTCC TGCACGCTTC CCTTGATTCT
501     GCTCCTGAGC CTATGGTAG
25

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**Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF  $\alpha 3$  receptor sequence)**

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1      ERRRNTIAPN CALPPVAPNC LELRRLCFSD PLCRSRLVDF QTHCHPMIDIL
30
30      51   GTCATEQSRC LRAYLGLIGT AMTPNFVSNV NTSVALSCTC RGSGNLQEEC
101    EMLEGFFSHN PCLTEAIAAK MRFHSQLFSQ DWPHPTFAVM AHQNENPAVR
35      151  PQPWVPSLFS CTLPLILLLS LW

```

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors

**Figure I - SEQ ID NO:1**

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT  
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC  
 101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG  
 151 TGCCAGGCTG ATCCCACCTG CAGTGCTGCC TACCACCACC TGGATTCTG  
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGGAGCCT TCGGTCCCTG  
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC  
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCCAG GTTGCCTGCT TGGAcATCTA  
 351 TTGGACCGTT CACCGTGCC GCAGCCTTGG TAACTATGAG CTGGATGTCT  
 401 CCCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC  
 451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT  
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG  
 551 AGGCGTGTCT CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG  
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT  
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA  
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGCCCCCCTA CTGCCTGGAG  
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAAGATCAC GCCTGGTCCA  
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG  
 851 AGCAGTCCAG ATGTCTACGA GCATACTGG GGCTGATTGG GACTGCCATG  
 901 ACCCCCAACT TTGTCAAGCAA TGTCAACACC AGTGTGCTTAAGCTGCAC  
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT  
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT  
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTGCTGT  
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC  
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

**Figure 2 - SEQ ID NO:2**

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK  
 51 CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG  
 101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL  
 151 KLNMLKPDSL LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL  
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCL  
 251 LRLLCFSDPN CRSRLVDFQT HCHPMIDILGT CATEQSRLCLR AYLGLIGTAM  
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR  
 351 FHSQQLFSQDW PHPTFAVMAM QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

**Figure 3 - SEQ ID NO:3**

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT  
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC  
 101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG  
 151 TGCCAGGCTG ATCCCACCTG CAGTGATGCC TACCACCACC TGGATTCCCTG  
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG  
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC  
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAAG GTTGCCTGCT TGGAcATCTA  
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT  
 401 CCCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC  
 451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT  
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG  
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG  
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT  
 651 GTGCCCATGT GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA  
 701 CCATCGCCCC CAACTGCGCG CTGCCGCCTG TGGCCCCAA CTGCCTGGAG  
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA  
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG  
 851 AGCAGTCCAG ATGTCTACGA GCATACTGG GGCTGATTGG GACTGCCATG  
 901 ACCCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCT TAAGCTGCAC  
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT  
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT  
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTGCTGT  
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC  
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

**Figure 4 - SEQ ID NO:4**

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK  
 51 CQADPTCSDA YHLDSDCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG  
 101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL  
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL  
 201 LTFFEKAEEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCL  
 251 LRRLCFSDPL CRSRLVDFQT HCHPMIDILGT CATEQSRLCLR AYLGLIGTAM  
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR  
 351 FHSQLFSQDW PHPTFAVMAM QNENPAVRPQ PWVPSLFSCT LPLILLLSLW .

**Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF  $\alpha 3$  receptor)**

1       GAGGCCGGC GCAACACCAT CGCCCCAAC TGCGCGCTGC CGCCTGTGGC  
5  
51      CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTGCA  
101     GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA  
10      151     GGAACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGCT  
201     GATTGGGACT GCCATGACCC CCAACTTGT CAGCAATGTC AACACCAGTG  
251     25      TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT  
301     301     GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT  
351     351     TGCAGCTAAG ATGCGTTTC ACAGCCAAC TTTCTCCAG GACTGGCCAC  
20      401     401     ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG  
451     451     CCACAGCCCT GGGTGCCCTC TCTTTCTCC TGCACGCTTC CCTTGATTCT  
501     501     GCTCCTGAGC CTATGGTAG  
25

**Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF  $\alpha 3$  receptor sequence)**

1       ERRRNTIAPN CALPPVAPNC LELRLLCFSD PLCRSRLVDF QTHCHPMIDIL  
30  
51      51      GTCATEQSRC LRAYLGLIGT AMTPNFVSNV NTSVALSCTC RGSGNLQEEC  
101     101     EMLEGFFSHN PCLTEAIAAK MRFHSQLFSQ DWPHPTFAVM AHQNENPAVR  
35      151     35      PQPWVPSLFS CTLPLILLLS LW

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors